

Gencore version 5.1.4-p5-4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

Om nucleic - nucleic search, using sw model

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Run on: May 16, 2003, 15:44:37 ; Search time 401.589 seconds
 (without alignments)
 1449.381 Million cell updates/sec

Title: US-10-052-092-15
 Perfect score: 20

Sequence: 1 caaggccagagatgtg 20
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
 Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba:
 2: gb_htg:
 3: gb_in:
 4: gb_cm:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_pl:
 9: gb_pr:
 10: gb_rst:
 11: gb_sts:
 12: gb_sy:
 13: gb_un:
 14: gb_vl:
 15: em_ba:
 16: em_fun:
 17: em_hun:
 18: em_in:
 19: em_mu:
 20: em_om:
 21: em_or:
 22: em_ov:
 23: em_pat:
 24: em_ph:
 25: em_pi:
 26: em_ro:
 27: em_sts:
 28: em_un:
 29: em_vl:
 30: em_htg_hum:
 31: em_htg_inv:
 32: em_htg_other:
 33: em_htg_mus:
 34: em_htg_pin:
 35: em_htg_rid:
 36: em_htg_mau:
 37: em_htg_vrt:
 38: em_sy:
 39: em_htg_o_hum:
 40: em_htg_o_mus:
 41: em_htg_o_other:

No.	Result	Score	Query	Match	Length	DB	ID	Description
C	1	20	100.0	26	6	E13443		E13443 PCR primer
C	2	20	100.0	144	9	S80316		S80316 oestrogen r
C	3	20	100.0	392	9	AF120105		AF120105 Homo sapi
C	4	20	100.0	521	6	AX004781		AX004781 Sequence
C	5	20	100.0	539	6	AX004793		AX004793 Sequence
C	6	20	100.0	566	6	AX004790		AX004790 Sequence
C	7	20	100.0	1223	6	AX066401		AX066401 Sequence
C	8	20	100.0	1237	9	HSERI3		AP123496 Homo sapi
C	9	20	100.0	1374	6	AX066402		AX066402 Sequence
C	10	20	100.0	1788	4	SSEREC		Z37167 S. scrofa mR
C	11	20	100.0	1788	6	AX11751		AX411751 Sequence
C	12	20	100.0	1966	4	OAESTREC		Z49257 O. aries mRN
C	13	20	100.0	2092	6	AX74709		AX47470 Sequence
C	14	20	100.0	2092	6	T08538		T08538 Sequence 1
C	15	20	100.0	2092	9	HUMERMCF		M12674 Human estro
C	16	20	100.0	2106	9	HSU47678		U47678 Human 80 kD
C	17	20	100.0	2322	6	A42099		AA2099 Sequence 1
C	18	20	100.0	3746	4	AF124093		AT124093 Equus cab
C	19	20	100.0	4963	6	AR029418		AR029418 Sequence
C	20	20	100.0	4963	6	I15368		I15368 Sequence 16
C	21	20	100.0	4963	6	I56760		I56760 Sequence 9
C	22	20	100.0	5653	4	AY03393		AY03393 Ovis arie
C	23	20	100.0	6450	6	ARL35385		ARL35385 Sequence
C	24	20	100.0	6450	9	HSERR		X13635 Human mRNA
C	25	20	100.0	6610	12	AF061181		AF06111 Mammalian
C	26	20	100.0	6639	6	AX128351		AX128351 Sequence
C	27	20	100.0	6695	6	AX128347		AX128347 Sequence
C	28	20	100.0	6695	6	AX128353		AX128353 Sequence
C	29	20	100.0	6695	6	AX128354		AX128354 Sequence
C	30	20	100.0	6801	6	AX128355		AX128355 Sequence
C	31	20	100.0	6818	6	AX128346		AX128346 Sequence
C	32	20	100.0	6833	6	AX128349		AX128349 Sequence
C	33	20	100.0	6900	6	AX128341		AX128341 Sequence
C	34	20	100.0	6956	6	AX128348		AX128348 Sequence
C	35	20	100.0	7038	6	AX128342		AX128342 Sequence
C	36	20	100.0	73687	9	AL509393		AL509393 Human DNA
C	37	20	100.0	16237	6	AX232505		AX232505 Sequence
C	38	20	100.0	349980	6	AX232503		AX232503 Sequence
C	39	20	100.0	349980	6	AX453703		AX453703 Sequence
C	40	18.4	92.0	748	4	CFA313195		ATJ1195 Canis fam
C	41	18	90.0	20000	2	AC007355		AC007355 Homo sapi
C	42	18	90.0	243358	2	AC110814		AC110814 Homo sapi
C	43	17.4	87.0	965989	2	AC125306		AC125306 Rattus no
C	44	17.4	87.0	146067	2	OSJN00150		AL662948 Oryza sat
C	45	17.4	87.0	160889	2	AC109098		AC109098 Rattus no

ALIGNMENTS

COMMENT	NIPPON BIO SERAPIT KK						
OS	38	a	48	c	40	g	
OC	Artificial sequences.						
PN	JP 1997187299-A/5						
PD	22-JUN-1997						
PF	05-JAN-1996 JP 1996027222						
PT	KIMOTO YASUHIKO						
PC	C12Q1/68,C07H21/04,C12N15/09;						
CC	strandedness: Single;						
CC	topology: Linear;						
CC	hypothetical: No;						
CC	anti sense: Yes;						
FH	KEY location/Qualifiers						
FT	source	1.	.26				
FT		/organism='Artificial sequences' FT					
FT	misc_feature	1.	.26	/note='PCR primer E-7'.			
FEATURES		location/Qualifiers					
SOURCE		1.	.25	/organism="unidentified"			
BASE COUNT	2	a	8	c	5	g	
ORIGIN		8	9	t	11	t	
Query Match	100.0%	Score	20;	DB	6;	Length	144;
Best Local Similarity	100.0%	Pred.	No.	6;			
Matches	20;	Conservative	0;		Mismatches	0;	
Db	6	CAAGGCCAGAGATGATG	25				
RESULT	3						
S80316	AF120105						
DEFINITION	Homo sapiens alternatively-spliced estrogen receptor alpha mRNA, partial cds.						
ACCESSION	AF120105						
VERSION	AF120105.1						
KEYWORDS	GI:4567039						
ORGANISM	Homo sapiens						
REFERENCE	Bukayto; Metzger; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 332)						
AUTHORS	Campbell-Thompson, M.L.						
TITLE	Direct Submission						
JOURNAL	Submitted (11-JAN-1999) Medicine, University of Florida, Box 100214						
FEATURES	Gastroenterology, Gainesville, FL 32667, USA						
SOURCE	Location/Qualifiers						
CDS	1.	.392					
	/organism="Homo sapiens"						
	/db_xref="taxon:9606"						
	/chromosome="6"						
	/map="6q25.1"						
	/sex="male"						
	/cell_type="colon adenocarcinoma"						
	<1.	.343					
	/note="steroid hormone receptor; missing exon 5"						
	/codon_start=2						
	/product="alternatively-spliced estrogen receptor alpha"						
	/protein_id="AA23556.1"						
	/db_xref="GI:14567040"						
	/translation="RGRGRMVKHRQRDODGEERGEVGSAGDRANTWPSPLMRSK KNSLALSLTADQMSAIIADDAPPLISEYDTPFSPASMGMLNLADRELVMINW AKRVPGTTRN"						
	25						
	/note="compared to wild type sequence deposited in GenBank Accession Number X03635"						
	/replace="a"						
	variation						
BASE COUNT	97	a	92	c	124	g	
ORIGIN		97	92	c	124	g	
Query Match	100.0%	Score	20;	DB	9;	Length	392;
Best Local Similarity	100.0%	Pred.	No.	6.3;			
Matches	20;	Conservative	0;		Mismatches	0;	
Db	28	CAAGGCCAGAGATGATG	47				
RESULT	4						
AX004781	AF004781						
LOCUS	Sequence 1 from Patent WO991785.						
DEFINITION	521 bp DNA linear						
ACCESSION	AX004781						
VERSION	AX004781.1						
KEYWORDS	GI:9928194						
SOURCE	unidentified.						
ORGANISM	unclassified.						
REFERENCE	1 (bases 1 to 521)						
FEATURES	/gene="oestrogen receptor, delta 4/7 ER"						
SOURCE	1.	.135					
	/partial						
	/gene="oestrogen receptor, delta 4/7 ER"						
	/note="this sequence comes from Fig. 3; delta 4/7 ER"						
	/codon_start=1						
	/product="oestrogen receptor"						
	/protein_id="AB3990.1"						
	/db_xref="GI:1246087"						
	/translation="KKRKRDRDGEGRDPDGQGRDPAAAPAAAGPAPPHPLPHQAE						

AUTHORS McGregor, D.
 TITLE Chimeric binding peptide library screening method
 JOURNAL Patent: WO 9911785-A 1 11-MAR-1999;
 MCGREGOR DUNCAN (GB); ROMPT RESEARCH SERVICES LIMIT (GB)
 FEATURES Location/Qualifiers
 source
 1. .521
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="Recombinant human oestrogen"
 CDS
 41. .124
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC04912.1"
 /db_xref="GI:9928195"
 /translation="MKTILPAAAGILLAAQPMAMAQVQLQ"
 BASE COUNT 153 a 109 c 155 g 104 t
 ORIGIN Query Match 100.0%; Score 20; DB 6; Length 521;
 Best Local Similarity 100.0%; Pred. No. 6; 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCAGAGAGATG 20
 Db 427 CAAGGCCAGAGAGATG 446
 RESULT 5
 AX004793 AX004793 539 bp DNA linear PAT 24-AUG-2000
 LOCUS Sequence 13 from Patent WO9911785.
 DEFINITION Accession AX004793
 VERSION AX004793.1 GI:9928204
 KEYWORDS
 SOURCE
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 539)
 AUTHORS McGregor, D.
 TITLE Chimeric binding peptide library screening method
 JOURNAL Patent: WO 9911785-A 13 11-MAR-1999;
 MCGREGOR DUNCAN (GB); ROMPT RESEARCH SERVICES LIMIT (GB)
 FEATURES
 source
 1. .539
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="Recombinant human oestrogen"
 CDS
 41. .431
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC04917.1"
 /db_xref="GI:9928205"
 /translation="MKTILPAAAGILLAAQPMAMAEMSAKERYCVCNDYASGH
 IGVWSCGECKAKFERSIQHENDMCPATNQCIDKRRRSCQAGRKKCIEVGMKGG
 IRDRRRGMLMKRDRDGEGRKEVGGGGSGSAQPAIQLAAN"
 BASE COUNT 148 a 118 c 165 g 108 t
 ORIGIN Query Match 100.0%; Score 20; DB 6; Length 539;
 Best Local Similarity 100.0%; Pred. No. 6; 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCAGAGAGATG 20
 Db 385 CAAGGCCAGAGAGATG 404
 RESULT 6
 AX004790 AX004790 566 bp DNA linear PAT 24-AUG-2000
 LOCUS Sequence 10 from Patent WO9911785.
 DEFINITION Accession AX004790
 VERSION AX004790.1 GI:9928202
 KEYWORDS
 SOURCE
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 566)
 AUTHORS McGregor, D.
 TITLE Chimeric binding peptide library screening method
 JOURNAL Patent: WO 9911785-A 10 11-MAR-1999;
 MCGREGOR DUNCAN (GB); ROMPT RESEARCH SERVICES LIMIT (GB)
 FEATURES
 source
 1. .566
 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="Recombinant human oestrogen"
 CDS
 41. .124
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC04916.1"
 /db_xref="GI:9928203"
 /translation="MKTILPAAAGILLAAQPMAMAQVQLQ"
 BASE COUNT 164 a 118 c 169 g 115 t
 ORIGIN Query Match 100.0%; Score 20; DB 6; Length 566;
 Best Local Similarity 100.0%; Pred. No. 6; 4; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCAGAGAGATG 20
 Db 427 CAAGGCCAGAGAGATG 446
 RESULT 7
 AX066401 AX066401 1223 bp DNA linear PAT 24-JAN-2001
 LOCUS Sequence 1 from Patent WO0100823.
 DEFINITION Accession AX066401
 VERSION AX066401.1 GI:12344111
 KEYWORDS
 SOURCE
 ORGANISM human.
 REFERENCE 1 (bases 1 to 1223)
 AUTHORS Gannon, F.; Dengler, S. and Flouriot, G.
 TITLE Novel isoforms of the human estrogen receptor- γ (a)
 JOURNAL Patent: WO 0100823-A 1 04-JAN-2001;
 EUROPEAN MOLECULAR BIOLOGY LABORATORY (DE)
 FEATURES
 source
 1. .1223
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 303 a 316 c 341 g 263 t
 ORIGIN Query Match 100.0%; Score 20; DB 6; Length 1223;
 Best Local Similarity 100.0%; Pred. No. 6; 7; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCAGAGAGATG 20
 Db 236 CAAGGCCAGAGAGATG 255
 RESULT 8
 HSSR13 HSSR13 1237 bp DNA linear PRI 07-APR-2000
 LOCUS Homo sapiens estrogen receptor alpha (ESR1) gene, exon 4.
 DEFINITION
 ACCESSION AF123496
 VERSION AF123496.1 GI:5821720
 KEYWORDS
 SEGMENT 3 of 7
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1237)
schubert,E.L., Lee,M.K., Newman,B. and King,M.C.
TITLE Single nucleotide polymorphisms (SNPs) in the estrogen receptor
gene and breast cancer susceptibility
J. Steroid Biochem. Mol. Biol. 71 (1-2), 21-27 (1999)

JOURNAL MEDLINE
PUBLISHED 10619354
REFERENCE 2 (bases 1 to 1237)
Schubert,E.L., Lee,M.K. and King,M.-C.
AUTHORS
TITLE Direct Submission
SUBMITTED (26-JAN-1999) Medical Genetics, University of Washington,
1959 NE Pacific Street, Seattle, WA 98195-7720, USA

FEATURES source
JOURNAL
SUBMISSION
PUBLISHED 1. .1237
/organism="Homo sapiens"
<db_xref="taxon:9606"
/map="6q25"
350. .685
/genes="ESR1"
/number=4
BASE COUNT 369 a 218 c 285 g 364 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 1237;
Best Local Similarity 100.0%; Pred. No. 6.7; Matches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGAGATG 20
Db 390 CAAGGCCAGAGAGATG 409

RESULT 9
AX066402
LOCUS Sequence 2 from Patent WO0100823.
DEFINITION AX066402
ACCESSION AX066402.1
VERSION GI:12544112
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1374)
Gannon,F., Dengler,S. and Flouriot,G.
TITLE Novel isoforms of the human estrogen receptor - g(a)
JOURNAL Patent: WO 0100823-A 2, 04-JAN-2001;
EUROPEAN MOLECULAR BIOLOGY LABORATORY (DE)
FEATURES source
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 349 a 346 c 386 g 293 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1374;
Best Local Similarity 100.0%; Pred. No. 6.7; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGAGATG 20
Db 387 CAAGGCCAGAGAGATG 406

RESULT 10
SSSTRNC SSSTRNC
LOCUS SSSTRNC
DEFINITION S.SS.RNC mRNA for estradiol receptor.
ACCESSION Z31167

FEATURES source
JOURNAL
SUBMISSION
PUBLISHED 1. .1788
/organism="Sus scrofa"
<db_xref="taxon:9823"
/sex="Female"
/tissue_type="Uterus"
1. .1788
/codon_start=1
/product="estradiol receptor"
<db_xref="taxon:9823.1"
/db_xref="swiss-prote:Q29040"
/translation="MMTHTRKSGMHLHQIQLRQNLPLRNPQKIPLERPLGEGVY
DSKRPAVNYRGAVAYDVAASAPVGSGLAGPSEMAFGANGVWCGFQINS
VSPSPVLLHPPQPSPLPHQGQVPLHPSLPSVKAEGPAPYRPNSDRQG
GREKLASNDKSMSMASEKETVCAVCDNDAASGHYQWSICGCKAFKSIQHND
LYMPATNOCTDKNWKRCGACURKVKYDQKNGJRKDRGRGMRKKRDGE
RNKRAVPPGDDMSANUMPSLILKTKNPKPLSLRADOMKSLAEPPTITSEIDPT
RPISEASUNGMILNTADREINLDRNWKVWRVFIQDLSIHDQVILCWLAWLTIGLV
WRSMHEGKLUFPNILLDRNOKCVGSMVMTDMLAASSRFRMOMQKGRFVRQIK
LILSHFRKTMNGKMGMLYKNNKCNVPUYDILLEMIDAHRLHAPTNLGPPEDMSQ
OLATSGSPPSISLOMYTQEAEWPIT"

RESULT 11
AX411751
LOCUS AX411751
DEFINITION Sequence 1 from Patent WO02288175.
ACCESSION AX411751
VERSION AX411751.1 GI:21444272
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Champon,P. and Metzger,D.
TITLE Transgenic mouse for targeted recombination mediated by modified
Cre-er
JOURNAL Patent: WO 0228175-A 1 11-APR-2002;
FEATURES source
JOURNAL
SUBMISSION
PUBLISHED 1. .1788
/organism="Mus musculus"
<db_xref="taxon:10093"
/map="6q25"
350. .685
/genes="Cre-er"
/number=4
BASE COUNT 410 a 530 c 504 g 344 t
ORIGIN
Query Match 100.0%; Score 20; DB 4; Length 1788;
Best Local Similarity 100.0%; Pred. No. 6.8; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGAGATG 20
Db 801 CAAGGCCAGAGAGATG 820

VERSION M12674.1 GI:182192
 KEYWORDS estrogen receptor
 SOURCE Human breast cancer cell line MCF-7, cDNA to mRNA, clone OR8.
 ORGANISM Homo sapiens
 EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidei; Homo.
 REFERENCE 1 (bases 1 to 2092)
 Greene,G.L., Gilna,P., Waterfield,M., Baker,A., Hort,Y. and
 Shine,J.
 TITLE Sequence and expression of human estrogen receptor complementary
 DNA
 JOURNAL Science 231 (4742), 1150-1154 (1986)
 MEDLINE 8622297
 PUBMED 3753802
 FEATURES Location/Qualifiers
 Source
 1. .2092
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="6q24-q27"
 /cell_line="MCF-7"
 /cell_type="Mammary Carcinoma"
 /lab_host="Prokaryote"
 /tissue_lrb="Lambda gt1"
 1..2092
 /gene="ESR"
 <1..>2092
 /gene="ESR"
 /product="ER mRNA"
 293..2080
 /gene="ESR"
 /note="estrogen receptor"
 /codon_start=1
 /protein_id="AA553399.1"
 /db_xref="GDB:G00-119-120"
 /transliteration="MINTLHTRASGHALLHOIQLQNEELPLNRPOLKPLRPLGEVIL
 DESKPQVNYTPEGAYANAHANQYKSYCTGGRYGGSEAARFSGNGGERPPLNS
 VSPSPMLLHEPPOLSPPLQPAGQQPYLJENEGSYIVREKGPPAYRNDSNRQG
 GBRBLASTNDKGSNAMEAKERYCAVCDYASCHYQWSCGCKAFERSFGHND
 YKCPAHCOTDKERKSCAOCLRCYEVGMMGGTKDRGGMKRQRQDGCG
 RQEVGSGDGRKANWPEPIMARKSKRSKNSLAISIADONSAIDKEPPLVSDPT
 RPFSEASMMGLLTNLADBLVMTLNINAKRYPGFVDTLHDQPHLCAWILMIGLV
 WSMELHEKYLKAFLPNTLUDRNGKCYEGMTEIEMLAITSSPERMANIQCERWCKS
 ILLMSCVYFLSSELKSLLEKDHIRVWKTIPDLMILAMAGLILQOHQRIAQLL
 LILSHHRMSKGMBHLSMKCNVPLVYDILMELMDARHLHAPTSRGASVETDOS
 BASE COUNT 473 a 605 c 593 g 421 t
 ORIGIN 1 bp upstream of EcoRI site.

Query Match 100.0%; Score 20; DB 9; Length 2092;
 Best Local Similarity 100.0%; Precl. No. 6; 9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAGGCCAGAGATGTG 20
Db	1093	CAAGCCAGAGATGTG 1112

Search completed: May 17, 2003, 00:56:23
 Job time : 408.589 secs

GenCore version 5.1.4-p5, 4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on: May 16, 2003, 12:48:16 ; Search time 111.126 Seconds

(without alignments)

405.306 Million cell updates/sec

Title: US-10-052-092-15
 Perfect score: 20
 Sequence: caaagccgcaagagatgtg 20
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 2185239 seqs, 1125999159 residues
 total number of hits satisfying chosen parameters: 4370478
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

- 1: N_Geneseq101002,*
- 2: /SIDS2/geodata/geneseq/geneseq-emb1/NA1980.DAT:*
- 3: /SIDS2/geodata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SIDS2/geodata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SIDS2/geodata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SIDS2/geodata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SIDS2/geodata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SIDS2/geodata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SIDS2/geodata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SIDS2/geodata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SIDS2/geodata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SIDS2/geodata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SIDS2/geodata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SIDS2/geodata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SIDS2/geodata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SIDS2/geodata/geneseq/geneseq-emb1/NA1995.DAT:*
- 17: /SIDS2/geodata/geneseq/geneseq-emb1/NA1996.DAT:*
- 18: /SIDS2/geodata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SIDS2/geodata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SIDS2/geodata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SIDS2/geodata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SIDS2/geodata/geneseq/geneseq-emb1/NA2001.DAT:*
- 23: /SIDS2/geodata/geneseq/geneseq-emb1/NA2002.DAT:*
- 24: /SIDS2/geodata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match length	DB ID	Description
c 1	20	100.0	26	18	AAV00167
c 2	20	100.0	521	20	AAX17808
c 3	20	100.0	539	20	AXX77813
c 4	20	100.0	566	20	AAX37812
c 5	20	100.0	1223	22	AAFF924
c 6	20	100.0	1374	22	AAFF925
c 7	20	100.0	1380	22	AAFF919
c 8	20	100.0	1788	24	ABL57497
c 9	20	100.0	2092	8	AAV70880

SUMMARIES

RESULT	No.	Score	Query	Match length	DB ID	Description
1	20	100.0	26	18	AAV00167	Human oestrogen receptor; oestrogen receptor; ER protein C
2	20	100.0	521	20	AAX17808	SSR-LBD fusion pol
3	20	100.0	539	20	AXX77813	PhCMV*-1 promoter
4	20	100.0	566	20	AAX37812	CDDA encoding rabbit protein
5	20	100.0	1223	22	AAFF924	Rabbit progesteron
6	20	100.0	1374	22	AAFF925	PhCMV*-1; rabbit progesteron
7	20	100.0	1380	22	AAFF919	Rabbit progesteron
8	20	100.0	1788	24	ABL57497	Human estrogen receptor
9	20	100.0	2092	8	AAV70880	cDNA encoding human oestrogen receptor

ALIGNMENTS

RESULT	ID	AAV00167/C	AAV00167 standard; DNA; 26 BP.
1	XX	AAV00167;	AAV00167;
2	XX	23-MAR-1998	(first entry)
3	XX	DE	Human oestrogen receptor PCR antisense primer E-7.
4	XX	XX	PCR primer; human; progesterone receptor; oestrogen; CD8; glucagon; interleukin 2; insulin; parathyroid hormone; cholecytokinin; enkephalin; adrenocorticotrophic hormone; thyroid stimulatory hormone; detection; diagnosis; ss.
5	XX	OS	Synthetic.
6	XX	OS	Homo sapiens.
7	XX	PN	JPO9187299-A.
8	XX	PD	22-JUL-1997.
9	XX	PP	05-JAN-1996; 96JP-002722.
10	XX	PR	05-JAN-1996; 96JP-002722.
11	XX	PA	(NIBI-) NIPPON BIOTHERAPY KK.
12	XX	DR	WPI; 1997-419410/39.
13	XX	PT	Polymerase chain reaction primers for detection of mRNA encoding various human protein(s) - e.g. cbs, interleukin-2, parathyroid

PT hormone, adrenocorticotrophic hormone and thyroid stimulating
 PT hormone
 XX
 PS Claim 1; Page 2; 4pp; Japanese.
 XX
 CC The present sequence represents a novel polymerase chain reaction
 CC (PCR) primer. The PCR primers of the present specification are used
 CC in the detection of mRNA encoding various human proteins. The mRNA
 CC can be detected in a single cell.
 XX
 SQ Sequence 26 BP; 2 A; 8 C; 5 G; 11 T; 0 other;
 Query Match 100.0%; Score 20; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCGAGAGATG 20
 Db 20 CAAGGCCGAGAGATG 1

RESULT 2
 ID AAX37808 standard; DNA; 521 BP.
 XX
 AC AAX37808;
 XX DT 09-JUL-1999 (first entry)
 XX DE pDM12 oestrogen receptor DNA binding domain fusion protein DNA.
 XX KW Peptide display carrier package; PDCP; chimeric protein; fusion protein;
 KW screening; library; secreted peptide; oestrogen receptor;
 KW DNA binding domain; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX FH Location/Qualifiers
 PH CDS 41..475
 FT /tag= a
 FT /product= "oestrogen receptor DNA binding domain
 FT fusion protein 5'-end"
 XX PN WO9911785-A1.
 XX PD 11-MAR-1999.
 XX PR 02-SEP-1998; 98WO-GB02630.
 XX PR 02-SEP-1997; 97GB-0018455.
 XX PR (RONE-) ROWETT RES SERVICES LTD.
 PI McGregor D;
 XX DR WPI; 1999-302254/25.
 DR P-PSDB; AAY08223.
 XX PT New peptide display carrier package useful for screening nucleotide
 PT libraries for sequences that encode peptides of interest
 XX PS Example 1; Fig 1; 103pp; English.
 XX This invention describes a novel peptide display carrier package (PDCP),
 CC comprising a recombinant polynucleotide-chimeric protein complex, for
 CC the isolation of peptide-encoding nucleic acid sequences from a DNA
 CC expression library. The PDCP comprises a recombinant
 CC polynucleotide-chimeric protein complex, where (a) the chimeric protein
 CC has a nucleotide binding portion (NBP) and a target peptide portion
 CC (TPP); (b) the recombinant polynucleotide comprises a specific sequence
 CC motif which is specifically bound by the NBP; and (c) at least the
 CC chimeric protein-encoding portion of the polynucleotide not bound by
 CC the NBP is protected by a binding moiety. The PDCP is used in the
 CC method for screening nucleotide libraries for sequences that encode
 CC peptides of interest. Unlike prior art, the invention provides a method
 CC to produce a peptide library where the DNA is protected from degradation,
 CC and which allows production of secreted peptides with a free carboxyl
 CC terminus. This sequence encodes a fusion protein fragment used in the
 CC method of the invention.
 XX SQ Sequence 521 BP; 153 A; 109 C; 155 G; 104 T; 0 other;
 Query Match 100.0%; Score 20; DB 20; Length 521;
 Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCCGAGAGATG 20
 Db 427 CAAGGCCGAGAGATG 446

RESULT 3
 ID ARX37813 standard; DNA; 539 BP.
 XX AC ARX37813;
 XX DT 09-JUL-1999 (first entry)
 XX DE pDM16 oestrogen receptor DNA binding domain fusion protein DNA.
 XX KW Peptide display carrier package; PDCP; chimeric protein; fusion protein;
 KW screening; library; secreted peptide; oestrogen receptor;
 KW DNA binding domain; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX FH Location/Qualifiers
 PH CDS 41..481
 FT /tag= a
 FT /product= "Oestrogen receptor fusion protein"
 XX PN WO9911785-A1.
 XX PD 11-MAR-1999.
 XX PR 02-SEP-1998; 98WO-GB02630.
 XX PR 02-SEP-1997; 97GB-0018455.
 XX PA (RONE-) ROWETT RES SERVICES LTD.
 PI McGregor D;
 XX DR WPI; 1999-302254/25.
 DR P-FDDB; AAY08228.
 XX PT New peptide display carrier package useful for screening nucleotide
 PT libraries for sequences that encode peptides of interest
 XX PS Example 5; Fig 5; 103pp;
 XX This invention describes a novel peptide display carrier package (PDCP),
 CC comprising a recombinant polynucleotide-chimeric protein complex, for
 CC the isolation of peptide-encoding nucleic acid sequences from a DNA
 CC expression library. The PDCP comprises a recombinant
 CC polynucleotide-chimeric protein complex, where (a) the chimeric protein
 CC has a nucleotide binding portion (NBP) and a target peptide portion
 CC (TPP); (b) the recombinant polynucleotide comprises a specific sequence
 CC motif which is specifically bound by the NBP; and (c) at least the
 CC chimeric protein-encoding portion of the polynucleotide not bound by
 CC the NBP is protected by a binding moiety. The PDCP is used in the
 CC method for screening nucleotide libraries for sequences that encode
 peptides of interest. Unlike prior art, the invention provides a method

CC to produce a peptide library where the DNA is protected from degradation,
 CC and which allows production of secreted peptides with a free carboxy
 CC terminus. This sequence encodes a fusion protein fragment used in the
 CC method of the invention.

XX Sequence 539 BP; 148 A; 118 C; 165 G; 108 T; 0 other;

SQ Query Match 100.0%; Score 20; DB 20; Length 539;

Best Local Similarity 100.0%; Pred. No. 2.4; 0; Mismatches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 CAAGCCGAGAGATGTC 20
 Db 385 CAAGGCCAGAGATGTC 404

RESULT 4

AAX38812
 ID AAX38812 standard; DNA; 566 BP.

XX AAX38812;

AC AAX38812;

DT 09-JUL-1999 (first entry)

XX DE PDML4 oestrogen receptor DNA binding domain fusion protein DNA.

XX KW Peptide display carrier package; PDCP; chimeric protein; fusion protein;

KW screening; library; secreted peptide; oestrogen receptor;

KW DNA binding domain; ss.

OS Synthetic.

OS Homo sapiens.

XX FH Location/Qualifiers

FT CDS 41..475

/*tag= a
 /product= "oestrogen receptor fusion Protein"

FT

PF 02-SEP-1998; 98WO-GB02630.

XX PN WO9911785-A1.

XX PR 11-MAR-1999.

XX PD 04-JUN-2001.

XX PT XX

XX PR 02-SEP-1997; 97GB-0018455.

XX PA (RONG-) ROWENT RSS SERVICES LTD.

XX PI McGregor D;

XX DR WPI; 1999-303254/25.

DR -PSDB; AAY08227.

XX PT New peptide display carrier package useful for screening nucleotide

PT libraries for sequences that encode peptides of interest

XX PS Example 4; Fig 4; 103pp; English.

XX CC This invention describes a novel peptide display carrier package (PDCP),

CC comprising a recombinant polynucleotide-chimeric protein complex for

CC the isolation of peptide-encoding nucleic acid sequences from a DNA

CC expression library. The PDCP comprises a recombinant

CC polynucleotide-chimeric protein complex, where (a) the chimeric protein

CC has a nucleotide binding portion (NBP) and a target peptide portion

CC (NPP); (b) the recombinant polynucleotide comprises a specific sequence

CC motif which is specifically bound by the NBP; and (c) at least one

CC chimeric protein-encoding portion of the polynucleotide not bound by

CC the NBP is protected by a binding moiety. The PDCP is used in the

CC method for screening nucleotide libraries for sequences that encode

CC peptides of interest. Unlike prior art, the invention provides a method

CC to produce a peptide library where the DNA is protected from degradation,

CC and which allows production of secreted peptides with a free carboxy

CC terminus. This sequence encodes a fusion protein fragment used in the

CC method of the invention.

XX Sequence 566 BP; 164 A; 118 C; 169 G; 115 T; 0 other;

SQ Query Match 100.0%; Score 20; DB 20; Length 566;

Best Local Similarity 100.0%; Pred. No. 2.4; 0; Mismatches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGATGTC 20
 Db 236 CAAGGCCAGAGATGTC 255

RESULT 5

AAR29924
 ID AAR29924 standard; DNA; 1223 BP.

XX AAR29924;

AC AAR29924;

DT 04-APR-2001 (first entry)

XX DE Human estrogen receptor alpha isoform #1 DNA.

XX KW Human; estrogen receptor alpha; cancer; osteoporosis; bone;

XX KW Alzheimer's; cardiovascular; ds.

XX OS Homo sapiens.

XX PN WO200100823-A1.

XX PD 04-JUN-2001.

XX PT 27-JUN-2000; 2000WO-EP05981.

XX PR 29-JUN-1999; 99IT-MI01433.

XX PA (EURO-) EURO MOLECULAR BIOLOGY LAB.

XX PT Novel isoforms of human estrogen receptor alpha useful for preparing

PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease and cardiovascular diseases

XX DR WPI; 2001-137955/14.

XX PT Cannon F, Dengler S, Flouriot G;

XX DR

XX PA (EURO-) EURO MOLECULAR BIOLOGY LAB.

XX PT Novel isoforms of human estrogen receptor alpha useful for preparing

PT therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease and cardiovascular diseases

XX PS Claim 1; Pag e44; 53pp; English.

XX CC The present invention relates to a human estrogen receptor

CC (ER)-alpha isoform. Molecules which modulate the activity of

CC the estrogen receptor are useful for the preparation of therapeutic

CC agents for treating cancer, osteoporosis and other bone disorders,

CC Alzheimer's disease and cardiovascular diseases.

XX SQ Sequence 1223 BP; 303 A; 316 C; 341 G; 263 T; 0 other;

XX PS Query Match 100.0%; Score 20; DB 22; Length 1223;

XX CC Best Local Similarity 100.0%; Pred. No. 2.7; 0; Mismatches 0; Indels 0; Gaps 0;

CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 CAAGGCCAGAGATGTC 20
 Db 236 CAAGGCCAGAGATGTC 255

RESULT 6

AAR29925
 ID AAR29925 standard; DNA; 1374 BP.

XX AC AAR29925;

XX DT 04-APR-2001 (first entry)

XX

The present sequence is the coding sequence of the human nuclear oestrogen receptor alpha (I). The invention relates to a non-human metazoan organism, especially a transgenic mouse, characterised in that at least one cell comprises: (i) a fusion protein formed from a recombinase (Cre), a hinge region (preferably derived from human (I)), and a modified ligand binding domain (LBD) of a nuclear oestrogen receptor, such as (I), its fragment or variant; and (ii) one or more genes or DNA sequences of interest belonging to the genome of the organism, into which one or more recognition sites of the recombinase protein are inserted. The (I) LBD domain is preferably modified by a G51R, G400W, or M543V/L544A mutation. The fusion protein has negligible, or even zero, recombinase activity in the presence of a natural ligand such as oestradiol; but recombinase activity is induced by a small quantity of a synthetic ligand that has anti-oestrogenic activity, e.g. tamoxifen or 4-hydroxytamoxifen. The metazoan organism or its cells, such as epidermal cells, hepatocytes or adipocytes, are useful in carrying out a spatiotemporally controlled site-specific recombination of a DNA sequence of interest in its natural chromatin environment. It is also used in screening of medicaments for pathological conditions associated with an alteration of the expression and/or function of the DNA sequence of interest, such as skin cancer, inflammation, diabetes, alopecia, obesity, or in promoting hepatic regeneration.

RESULT 9

Sequence	1788	BP;	418	A;	515	C;	508	G;	347	T;	0	other;
Best Match	100.0%		Score	20;	DB	24;	Length	1788;				
Matches	20;		Local Similarity	100.0%;	Pred.	No.	2.9;					
			Conservative	0;	Mismatches	0;						
					Indels	0;						
					Gaps	0;						
OY	1		CAAGGCCAGAGATGATG	20								
Db	801		CAAGGCCAGAGATGATG	820								

AC AANT0880
XX
AC AANT0880;
XX
DT 24-FEB-1991 (first entry)
DE cDNA encoding human oestrogen receptor protein.
XX
KW Human oestrogen receptor protein; ss cDNA; expression system; assay;
KW steroid receptor protein;
OS Homo sapiens.
XX
FF Key location/Qualifiers
FT CDS 293..1280
FT /*tag= a
XX
PN WO8705049-A.
XX
PD 27-AUG-1987.
XX
PF 18-FEB-1987; 87WO-US00341.
XX
PR 20-FEB-1986; 86US-0833829.
XX
PA (CALB-) CALIFORNIA BIOTECHNOLOGY INC.
XX
PI Shine J;
XX
DR WPI; 1987-250213/35.
DR P-PSDB; AAP70543.
PP Expression system for vertebrate steroid receptor protein - comprising
PT DNA sequence encoding the protein linked to control sequences in
eucaryotic hosts.

Disclosure; Fig. 1-1 - 1-2; 26pp; English.
 The cDNA can be used in an expression system to express human oestrogen receptor protein. The coding sequence is operably linked to control sequences compatible with eukaryotic host cells. This method allows expression under conditions which favour appropriate post-translational processing. It produces large amounts of purified protein useful in the design of agonist and antagonist cpd's., for the study of the mechanism of action of the steroid binding proteins in General, and for use in diagnostic assays for the proteins or antibodies to them. These assays are important in, eg the diagnosis of tumour sensitivities to steroid metabolism. Suitable host cells are VERO, CC HeLa and CHO cells.
 XX Sequence 2092 BP; 473 A; 607 C; 591 G; 421 T; 0 other;
 SQ Query Match 100.0%; Score 20; DB 8; Length 2092;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OQ 1 CAAGCGCAGAGAGATG 20
 Db 1093 CAAGGCCAGAGAGATG 1112
 |||||||
 RESULT 10
 AAC86920
 AAC86920 standard; cDNA; 2092 BP.
 ID AAC86920;
 XX AAC86920;
 AC AAC86920;
 DT 02-APR-2001 (first entry)
 DE Nucleotide sequence of the human oestrogen receptor cDNA.
 KW Ribozyme; oestrogen-dependent tumour; cell proliferation; glucocorticoid;
 KW DNA-binding domain; oestrogen receptor; cancer treatment; breast cancer;
 KW ss.
 OS Homo sapiens.
 XX PN WO20074485-A1.
 XX PR 04-JUN-1999; 99US-0137470.
 XX PA (TEXA) UNIV TEXAS.
 XX PI ROY AK, Lavrovsky Y, Tyagi RK, Song CS, Chatterjee B;
 DR WIT; 2001-051633/07.
 XX PT Ribozyme having a high substrate specificity for an mRNA encoding a
 PT DNA-binding domain of human estrogen receptor, useful for inhibiting
 PT estrogen-dependent tumour cell proliferation, particularly breast cancer
 PT
 XX Disclosure; Page 8-9; 49pp; English.
 CC The specification describes a ribozyme capable of inhibiting
 CC oestrogen-dependent tumour cell proliferation and having a high
 CC substrate specificity for an mRNA sequence encoding a DNA-binding
 CC domain of human estrogen receptor. The ribozyme is free of endonuclease
 activity for an mRNA having a DNA binding domain of a glucocorticoid.
 CC The oestrogen receptor site-specific ribozymes are useful for cancer
 CC treatment and therapies, especially for inhibiting oestrogen-dependent
 CC tumour cell proliferation, particularly breast cancer. The present
 CC sequence represents the human oestrogen receptor cDNA.
 XX

SQ	Sequence 2092 BP; 4/3 A; 605 C; 593 G; 421 T; 0 other;
Query Match	100.0%; Score 20; DB 22; Length 2092;
Best Local Similarity	100.0%; Pred. No. 3;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CAAGCGCAGAGAGATG 20
Db	1093 CAAGGCCAGAGAGATG 1112
RESULT 11	
ABU5100	
ID	ABL51900 standard; cDNA; 2092 BP.
XX	
AC	ABL51900;
XX	
DT	10-JUL-2002 (first entry)
DE	Human oestrogen receptor encoding cDNA SEQ ID NO:9.
XX	
KW	Target activated nucleic acid biosensor; signalling moiety; human;
KW	nucleic acid sensor; detection; engineering; drug optimisation;
KW	oestrogen receptor; gene; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key location/Qualifiers
FT	CDS 293..2080
FT	
FT	/product= "oestrogen receptor"
XX	
PN	WO200222882-A2.
XX	
PD	21-MAR-2002.
XX	
PF	13-SEP-2001; 2001WO-US288935.
XX	
PR	13-SEP-2000; 2000US-232454P.
XX	
PA	(ARCH-) ARCHEMIX CORP.
XX	
PT	Stanton M, Epstein D, Hamaguchi N;
XX	
DR	WPI; 2002-393977/42.
XX	
P-PSDB; ABB09265.	
XX	
PT	Nucleic acid sensor for detecting target molecule, comprises target nucleic acid activation site and optical signalling unit that changes its optical properties upon allosteric modulation sensor after recognition of target.
XX	
PS	Example 2; Page 75-76; 144PP; English.
XX	
CC	The present invention describes a nucleic acid sensor molecule (I) comprising a target molecule activation site comprising a structure that recognises a target molecule and an optical signalling unit including at least one nucleotide coupled to a signalling moiety that changes its optical properties upon allosteric modulation of (I), following recognition of the target molecule. (I) is useful for detecting a target molecule associated with a pathological condition or genetic alteration.
CC	(I) is useful for identifying a drug compound, by identifying a nucleic acid biosensor-based molecule profile of target molecules associated with a disease trait in a patient, administering a candidate compound to the patient, and monitoring changes in the profile. Alternately, the method involves identifying a number of pathway target molecules, administering a candidate compound to a patient having a disease trait, and monitoring changes in the structure, level or activity of two or more of the pathway target molecules using (I). The profile of target molecules or the changes in the structure is compared to the profile of a reference healthy or diseased population. (I) is useful in multiple assays, for the detection of target molecule. (I) is also useful in diagnostic applications and drug optimisation. The present sequence encodes the
CC	human oestrogen receptor, which is used in an example from the present invention.
CC	invention.
CC	invention.
SQ	Sequence 2092 BP; 473 A; 605 C; 593 G; 421 T; 0 other;
Query Match	100.0%; Score 20; DB 24; Length 2092;
Best Local Similarity	100.0%; Pred. No. 3;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CAAGCGCAGAGAGATG 20
Db	1093 CAAGGCCAGAGAGATG 1112
RESULT 12	
ABA01104	
ID	ABA01104 standard; cDNA; 2220 BP.
XX	
AC	ABA01104;
XX	
DT	01-FEB-2002 (first entry)
XX	
DE	Fused ER protein cDNA.
XX	
KW	Human; oestrogen receptor; ER; Eralpha; fusion; screening;
KW	sugar-binding protein; ss.
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Unidentified.
XX	
PN	JP2001238572-A.
XX	
PD	25-SEP-2001.
XX	
PF	23-MAR-2000; 2000JP-0082034.
XX	
PR	23-MAR-2000; 2000JP-0082034.
XX	
PA	(TOYM) TOYOB0 KK.
XX	
DR	WPI; 2002-003334/01.
XX	
P-PSDB; AAM51591.	
XX	
PT	Fusion protein for screening exogenous increation disturbance substances, comprises the fused estrogen receptor protein
XX	
PS	Claim 10; Page 9-10; 14pp; Japanese.
XX	
CC	The invention relates to a fused oestrogen receptor (ER) protein in which an ER protein is fused with a sugar-binding protein through a protease-resistant sequence. The fused ER protein can be used for screening exogenous increation disturbing substances. A polynucleotide encoding Eralpha was isolated from human cDNA by PCR.
CC	The present sequence encodes the fusion protein of the invention.
SQ	Sequence 2220 BP; 594 A; 562 C; 604 G; 460 T; 0 other;
Query Match	100.0%; Score 20; DB 24; Length 2220;
Best Local Similarity	100.0%; Pred. No. 3;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CAAGCGCAGAGAGATG 20
Db	1236 CAAGGCCAGAGAGATG 1255
RESULT 13	
AAX60628	
ID	AAX60628 standard; DNA; 2322 BP.
XX	
AC	AAX60628;
XX	
DT	03-AUG-1999 (first entry)

PN WO9429442-A.
XX
PD 22-DEC-1994.
XX
PP 14-JUN-1994; 94WO-US06734.
XX
PR 14 JUN 1993; 93US-0076327.
XX
PA (BARD) BASF AG.
XX
PI Buijard H, Gossen M, Salfeld JG, Voss JW;
XX
DR WPI; 1995-036472/05.
XX
PT Regulatory systems using tetracycline-controllable transactivator
PT (tTA) - useful for conditional inactivation or modulation of
PT gene expression in a host cell or animal
XX
PS Disclosure; Page 54-58; 103pp; English.
XX
CC The minimal promoter PhCMV*-1 is based on the human CMV
CC intermediate-early promoter (with enhancer region removed), fused
CC to a tetracycline operator, tetO. The promoter is used to
CC express tTA transactivator in host cells. In clone pBUD 3G4
CC (given in AAQ76269), cDNA for rabbit progesterone receptor is under
the control of PhCMV*-1.
XX
SQ sequence 4963 bp; 1259 A; 1298 C; 1280 G; 1126 T; 0 other;
Query Match 100.0%; Score 20; DB 16; length 4963;
Best Local Similarity 100.0%; Pred. No. 3; 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAGCGCAGAGATGATG 20
Db 1266 CAAGCGCAGAGATG 1285

Search completed: May 16, 2003, 15:58:25
Job time : 116.16 secs

Gencore version 5.1.4-p5-4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on:

May 16, 2003, 19:53:58 ; Search time 23.1788 Seconds

(without alignments)

264.618 Million cell updates/sec

Title: US-10-052-092-15
 Perfect score: 20
 Sequence: 1 caagcgccaaagatgtg 20

Scoring table: IDENTITY_NUC
 gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:
 5: /cgn2_6/ptodata/1/ina/PCMS_COMB.seq:
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Match Length	DB ID	Description
1	20	100.0	2322	3 US-08-564-264-2	Sequence 2, Appli
2	20	100.0	4963	1 US-08-076-726-16	Sequence 16, Appli
3	20	100.0	4963	1 US-08-200-452-9	Sequence 9, Appli
4	20	100.0	4963	2 US-08-481-970-9	Sequence 9, Appli
5	20	100.0	4963	2 US-08-897-719-9	Sequence 9, Appli
6	20	100.0	4963	4 US-09-163-269-9	Sequence 9, Appli
7	20	100.0	6450	4 US-09-041-866-34	Sequence 34, Appli
8	20	100.0	6450	4 US-08-453-988-1	Sequence 1, Appli
9	15.8	79.0	2328	1 US-08-688-649-38	Sequence 38, Appli
10	15.8	79.0	2328	4 US-09-715-524-B-1	Sequence 1, Appli
11	15.8	79.0	3499	1 US-07-966-218-2	Sequence 2, Appli
12	15.8	79.0	3499	1 US-08-424-931-2	Sequence 2, Appli
13	15.8	79.0	3499	2 US-08-556-55A-2	Sequence 2, Appli
14	15.8	79.0	3499	2 US-07-803-627-A-2	Sequence 2, Appli
15	15.8	77.0	1542	3 US-09-839-879-6	Sequence 6, Appli
16	15.4	77.0	3640	4 US-09-221-017-B-1047	Sequence 1047, Appli
17	15.4	76.0	3506	3 US-08-814-095-7	Sequence 7, Appli
18	15.2	76.0	737	2 US-08-861-549-2	Sequence 2, Appli
19	15.2	76.0	1308	1 US-08-518-878-B-57	Sequence 57, Appli
20	15.2	76.0	1308	2 US-08-807-861A-57	Sequence 57, Appli
21	15.2	76.0	1308	3 US-09-210-631-57	Sequence 57, Appli
22	15.2	76.0	1308	3 US-08-946-719-A-57	Sequence 57, Appli
23	15.2	76.0	3870	1 US-08-138-641-1	Sequence 1, Appli
24	15.2	76.0	3870	1 US-08-138-133-1	Sequence 1, Appli
25	15.2	76.0	3893	1 US-08-138-641-3	Sequence 3, Appli
26	15.2	76.0	3893	1 US-08-138-133-3	Sequence 3, Appli
27	15.2	76.0	4198	4 US-09-886-719-11	Sequence 11, Appli

ALIGNMENTS

28	14.8	74.0	575	4 US-09-385-982-450	Sequence 450, Appli
29	14.8	74.0	1776	4 US-09-149-476-59	Sequence 55, Appli
30	14.8	74.0	1791	4 US-09-149-476-226	Sequence 226, Appli
31	14.8	74.0	5455	1 US-09-342-930-1	Sequence 1, Appli
32	14.8	74.0	9848	4 US-09-385-222A-3	Sequence 3, Appli
33	14.8	74.0	10163	2 US-08-659-251-1	Sequence 1, Appli
34	14.8	74.0	10163	4 US-09-255-490-1	Sequence 1, Appli
35	14.8	74.0	10163	5 PCT-US96-114451	Sequence 1, Appli
36	14.4	72.0	810	4 US-09-230-041-1	Sequence 1, Appli
37	14.2	71.0	30	3 US-09-167-717-6	Sequence 6, Appli
38	14.2	71.0	750	3 US-09-167-717-4	Sequence 4, Appli
39	14.2	71.0	864	4 US-09-439-261-12	Sequence 12, Appli
40	14.2	71.0	864	4 US-09-227-613-13	Sequence 13, Appli
41	14.2	71.0	918	4 US-09-439-261-5	Sequence 5, Appli
42	14.2	71.0	918	4 US-09-227-613-5	Sequence 5, Appli
43	14.2	71.0	960	4 US-09-439-261-36	Sequence 36, Appli
44	14.2	71.0	960	4 US-09-227-613-35	Sequence 35, Appli
45	14.2	71.0	990	4 US-09-439-261-35	Sequence 35, Appli

NAME/KEY: misc.feature
 LOCATION: (1270-1284)
 OTHER INFORMATION: /note= "Linker peptide."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1285-2322)
 OTHER INFORMATION: /note= "Estrogen binding domain."
 ; US-08-564-264-2
 Query Match 100.0%; Score 20; DB 3; Length 2322;
 Best Local Similarity 100.0%; Pred. No. 0 53; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGCCCCAGAGATGTC 20
 Db 1335 CAAGCGCCAGAGATGAG 1354

RESULT 2
 US-08-076-726-16
 Sequence 16 Application US/08076726
 ; Patent No. 5,647,58
 GENERAL INFORMATION:
 ; APPLICANT: Gossen, Manfred
 APPLICANT: Buillard, Hermann
 APPLICANT: Saifeld, Jochen
 APPLICANT: Voss, Jeffrey
 TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic Cells by Tetracycline-responsive Promoters
 NUMBER OF SEQUNCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/260,452
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/076,327
 ATTORNEY/AGENT INFORMATION:
 NAME: Giulio A. DeConti, Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE DOCKET NUMBER: BRI-013CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 FAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4,963 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Human cytomegalovirus
 IMMEDIATE SOURCE:
 CLONE: pHD BGR4
 ; US-08-260-452-9
 Query Match 100.0%; Score 20; DB 1; Length 4963;
 Best Local Similarity 100.0%; Pred. No. 0 58; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGCGCCAGAGATGTC 20
 Db 1266 CAAGCGCCAGAGATGAG 1285

RESULT 4
 US-08-481-970-9
 Sequence 9 Application US/08481970
 ; Patent No. 5,853,110
 GENERAL INFORMATION:
 ; APPLICANT: Gossen, Manfred
 APPLICANT: Buillard, Hermann
 APPLICANT: Saifeld, Jochen
 APPLICANT: Voss, Jeffrey
 TITLE OF INVENTION: Animal Transgenic for a Tetracycline-controlled Transcri
 NUMBER OF SEQUNCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02109-1875

RESULT 3
 US-08-260-452-9
 Sequence 9 Application US/08260452
 ; Patent No. 5,650,298

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,970
 FILING DATE:
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/260,452
 FILING DATE: 14-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076,327
 FILING DATE: 14-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Giulio A. Deconti, Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: BBI-013CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4963 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 ORGANISM: Human cytomegalovirus
 IMMEDIATE SOURCE:
 CLONE: PUDH BGR4
; US-08-481-970-9

RESULT 5
 US-08-897-719-9
 ; Sequence 9, Application US/08897719
 ; Patent No. 5932927
 ; GENERAL INFORMATION:
 ; APPLICANT: Gossen, Manfred
 ; APPLICANT: Bujard, Hermann
 ; APPLICANT: Salfield, Jochen
 ; APPLICANT: Voss, Jeffrey
 TITLE OF INVENTION: Tight Control of Gene Expression in Eucaryotic
 TITLE OF INVENTION: Cells by Tetracycline-Responsive Promoters
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 60 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/163,269
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/481,970
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076,327
 FILING DATE: 14-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Giulio A. Deconti, Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: BBI-013CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
; US-08-897-719-9

RESULT 6
 US-09-163-269-9
 ; Sequence 9, Application US/09163269
 ; Patent No. 6252136
 ; GENERAL INFORMATION:
 ; APPLICANT: Gossen, Manfred
 ; APPLICANT: Bujard, Hermann
 ; APPLICANT: Salfield, Jochen
 ; APPLICANT: Voss, Jeffrey
 TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/163,269
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/481,970
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076,327
 FILING DATE: 14-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Giulio A. Deconti, Jr.
 REGISTRATION NUMBER: 31,503
 REFERENCE/DOCKET NUMBER: BBI-013CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4163 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double

MOLECULE TYPE: DNA (genomic)

ORGANISM: Human cytomegalovirus

IMMEDIATE SOURCE:
 CLONE: PUHD BGR4

US-09-163-269-9

RESULT 7

Query Match	100.0%	Score	20	DB	4	Length	4963
Best Local Similarity	100.0%	Pred.	No.	0.58;	0;	Mismatches	0;
Matches	20;	Conservative	0;			Indels	0;
QY	1	CAAGGCCAGAGATGATG	20			Gaps	0;
Db	1266	CAAGGCCAGAGATGATG	1285				

US-09-041-886-34

PATENT NO. 633872

GENERAL INFORMATION:

APPLICANT: BREDESEN, Dale E.

APPLICANT: RABIZADEH, Sharroz

TITLE OF INVENTION: Proapoptotic Peptides, Dependence NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122

COMPUTER READABLE FORM:
 COMPUTER TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/453,998
 FILING DATE: ZIN: 2005

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/161,064
 FILING DATE: 03-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: CHAPIN, MARILYN K.
 REGISTRATION NUMBER: 35,843
 REFERENCE/DOCKET NUMBER: 1037/98493
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3711
 TELEX: 6714227 CUSH
 FAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6450 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-453-998-1

RESULT 8

Query Match	100.0%	Score	20	DB	4	Length	6450
Best Local Similarity	100.0%	Pred.	No.	0.6;	0;	Mismatches	0;
Matches	20;	Conservative	0;			Indels	0;
QY	1	CAAGGCCAGAGATGATG	20			Gaps	0;
Db	1161	CAAGGCCAGAGATGATG	1180				

US-08-638-649-38

SEQUENCE CHARACTERISTICS:
 LENGTH: 38 base pairs
 TYPE: nucleic acid

GENERAL INFORMATION:
 PATENT NO. 5827716

APPLICANT: MAMONE, JOSEPH A.

TITLE OF INVENTION: MODIFIED POL-II TYPE DNA NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700

RESULT 9

Query Match	100.0%	Score	20	DB	4	Length	6450
Best Local Similarity	100.0%	Pred.	No.	0.6;	0;	Mismatches	0;
Matches	20;	Conservative	0;			Indels	0;
QY	1	CAAGGCCAGAGATGATG	20			Gaps	0;
Db	1161	CAAGGCCAGAGATGATG	1180				

US-09-041-886-34

Query Match

Best Local Similarity

Matches

QY

Db

US-09-163-269-9

Query Match

Best Local Similarity

Matches

QY

Db

US-09-041-886-34

Query Match

Best Local Similarity

Matches

QY

Db

CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 Z.I.P.: 90071-2006

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/688,649
 FILING DATE: Filed Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 220/281

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 38:
 LENGTH: 2328 base pairs
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-688-649-38

Query Match 79.0%; Score 15.8; DB 4; Length 2328;
 Best Local Similarity 89.5%; Pred. No. 57; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; General Information:
 SEQ 1 CAAGGCCAGAGATGAT 19
 Db 554 CAAGCGAGAGAGATGAT 572

RESULT 10

US-09-715-524B-1

Sequence 1, Application US/09/15524B
 Patent No. 6333183

GENERAL INFORMATION:
 APPLICANT: Evans, Steven
 APPLICANT: Manone, Steven
 APPLICANT: Davis, Maria
 APPLICANT: Connolly, Bernard

TITLE OF INVENTION: Improving Dideoxynucleotide-Triphosphate Utilization by Title of Invention: the Hyper-Thermophilic DNA Polymerase from the Archaeon Pyrococcus Furiosus

FILE REFERENCE: PB-9655

CURRENT APPLICATION NUMBER: US/09/15,524B
 CURRENT FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/167,066
 PRIOR FILING DATE: 1999-11-23

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1
 LENGTH: 2328
 TYPE: DNA
 ORGANISM: Pyrococcus furiosus

US-09-715-524B-1

Query Match 79.0%; Score 15.8; DB 4; Length 2328;
 Best Local Similarity 89.5%; Pred. No. 57; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; General Information:
 SEQ 1 CAAGGCCAGAGATGAT 19
 Db 777 CAAGCGAGAGAGATGAT 795

RESULT 11

US-07-966-278-2

Query Match 79.0%; Score 15.8; DB 1; Length 3499;
 Best Local Similarity 89.5%; Pred. No. 60; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; General Information:
 SEQ 1 CAAGGCCAGAGATGAT 19
 Db 777 CAAGCGAGAGAGATGAT 795

RESULT 12

US-08-424-921-2

Query Match 79.0%; Score 15.8; DB 1; Length 3499;
 Best Local Similarity 89.5%; Pred. No. 60; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; General Information:
 SEQ 1 CAAGGCCAGAGATGAT 19
 Db 777 CAAGCGAGAGAGATGAT 795

TITLE OF INVENTION: PURIFIED THERMOSTABLE PYROCOCCUS
 TITLE OF INVENTION: FURIOSUS DNA POLYMERASE I
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bingham & Fitting
 STREET: 1226 High Bluff Road, Suite 300
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92130
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,921
 FILING DATE: 19-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/803,627
 FILING DATE: 02-DEC-1991
 APPLICATION NUMBER: US 07/620,568
 FILING DATE: 03-DEC-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,073
 FILING DATE: 19-FEB-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/776,552
 FILING DATE: 15-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SMC010P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3499 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: 5' UTR
 LOCATION: 1..223
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 224..2551
 FEATURE:
 NAME/KEY: 3' UTR
 LOCATION: 2552..3499
 US-08-424-921-2

Query Match 79.0%; Score 15.8; DB 1; Length 3499;
 Best Local Similarity 89.5%; Pred. No. 60;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGGCCAGAGATGAT 19
 ||||| ||||||| |||||
 Db 777 CAAGCGAGAGAGATGAT 795

RESULT 13
 US-08-556-355A-2
 Sequence 2, Application US/08556355A
 ; Patent No. 5866395
 ; GENERAL INFORMATION:
 ; APPLICANT: MATUR, Eric J.
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington

Qy 1 CAAGGCCAGAGATGAT 19
 ||||| ||||||| |||||
 Db 777 CAAGCGAGAGAGATGAT 795

RESULT 14
 US-07-803-627A-2
 Sequence 2, Application US/07803627A
 ; General Information:
 ; APPLICANT: MATUR, Eric J.
 ; TITLE OF INVENTION: Purified Thermstable Pyrococcus
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington

TITLE OF INVENTION: furiosus DNA Polymerase I
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/556,355A
 FILING DATE: 13-NOV-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/424,921
 FILING DATE: 19-APR-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/803,627
 FILING DATE: 02-DEC-1991
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/779,846
 FILING DATE: 03-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. Paul
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 04121.004-02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)408-4000
 TELEFAX: (202)408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3499 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-556-355A-2

Query Match 79.0%; Score 15.8; DB 2; Length 3499;
 Best Local Similarity 89.5%; Pred. No. 60;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGGCCAGAGATGAT 19
 ||||| ||||||| |||||
 Db 777 CAAGCGAGAGAGATGAT 795

RESULT 14
 US-07-803-627A-2
 Sequence 2, Application US/07803627A
 ; General Information:
 ; APPLICANT: MATUR, Eric J.
 ; TITLE OF INVENTION: furiosus DNA Polymerase I
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington

STATE: D. C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/803,627A

FILING DATE: 02-DEC-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/776,552

FILING DATE: 14-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/657,073

FILING DATE: 19-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,568

FILING DATE: 03-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. Paul
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 04121.0004-00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3499 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-803-627A-2

Query Match 79.0%; Score 15.8; DB 2; Length 3499;
 Best Local Similarity 89.5%; Pred. No. 60; Mismatches 0;
 Matches 17; Conservative 0; Indels 2; Gaps 0;

QY 1 CAAGGCCAGAGATGAT 19
 DB 777 CAACGGAGAGAGAGAT 795

RESULT 15

US-09-089-879-6

Sequence 6, Application US/09089879
 Patent No. 611092

GENERAL INFORMATION:

APPLICANT: Williamson, Mark

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING DRILL1 AND USES THEREOF

FILE REFERENCE: 07334/078001

CURRENT APPLICATION NUMBER: US/09/089,879

CURRENT FILING DATE: 1998-06-03

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6
 LENGTH: 1542TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1542)
 OTHER INFORMATION: n = A,T,C or G

US-09-089-879-6

Dj 483 |||||||AAGCCGCAAGAGAGA 499
 |||||||AAGCCGCAAGAGAGA 499

Search completed: May 17, 2003, 03:41:13
 Job time : 30.1788 secs

Query Match 77.0%; Score 15.4; DB 3; Length 1542;
 Best Local Similarity 94.1%; Pred. No. 85; Mismatches 1;
 Matches 16; Conservative 0; Indels 0; Gaps 0;
 SEQ ID NO 2 AAGGCCAGAGAGATGA 18

GenCore version 5.1.4.p5_4578
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2003, 01:06:03 ; search time 48.3444 Seconds

(without alignments)
 33.646 Million cell updates/sec

Title: US-10-052-092-15

Perfect score: 20

Sequence: 1 caagcgcacagatgtg 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 810007 seqs, 64496991 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: Published_Applications_NA:*
2: /cgn2_6/ptodata/1/pupbna/rus07_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pupbna/us05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pupbna/us05_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pupbna/rus07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pupbna/PCTRS_PUBCOMB..seq:*
7: /cgn2_6/ptodata/1/pupbna/rus08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pupbna/rus08_PUBCOMB..seq:*
9: /cgn2_6/ptodata/1/pupbna/us09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pupbna/rus09_PUBCOMB..seq:*
11: /cgn2_6/ptodata/1/pupbna/rus10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pupbna/us10_PUBCOMB..seq:*
13: /cgn2_6/ptodata/1/pupbna/us10_PUB..seq:*
14: /cgn2_6/ptodata/1/pupbna/rus10_PUBCOMB..seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	20	100.0	20	9 US-10-052-092-15
2	20	100.0	392	9 US-10-052-092-4
3	20	100.0	1237	9 US-10-052-092-3
4	20	100.0	1788	9 US-10-052-092-24
5	20	100.0	1788	10 US-09-853-033-1
6	20	100.0	9	US-09-853-032-6
7	20	100.0	2092	9 US-09-952-680A-9
8	20	100.0	2106	9 US-10-052-092-5
9	20	100.0	4963	10 US-09-881-674-9
10	20	100.0	4963	10 US-09-892-227-9
11	20	100.0	6450	9 US-10-098-710-2
12	20	100.0	6450	9 US-10-081-563-1
13	20	100.0	6450	9 US-10-052-092-1
14	20	100.0	6450	9 US-10-052-092-7
15	20	100.0	6610	9 US-10-052-092-20
16	20	100.0	465337	10 US-09-933-267A-1
17	16.4	82.0	1978	9 US-10-052-092-23
c	18	15.8	79.0	10 US-09-864-671-33769
c	19	15.8	534	10 US-09-884-761-038

ALIGNMENTS

20	15.8	79.0	2454	9 US-10-050-036-176	Sequence 176, App	
21	15.8	79.0	2454	10 US-09-662-436-563	Sequence 563, App	
22	15.8	79.0	2480	9 US-10-050-036-548	Sequence 458, App	
C	23	15.4	77.0	2000	9 US-09-938-842A-2874	Sequence 2874, App
C	24	15.2	76.0	148	9 US-09-664-877-681	Sequence 681, App
C	25	15.2	76.0	183	10 US-09-920-300A-988	Sequence 988, App
C	26	15.2	76.0	183	12 US-10-033-528-888	Sequence 988, App
C	27	15.2	76.0	210	10 US-09-664-877-3406	Sequence 4369, App
C	28	15.2	76.0	395	9 US-09-918-995-4169	Sequence 1767, A
C	29	15.2	76.0	419	9 US-09-918-995-17697	Sequence 1775, A
C	30	15.2	76.0	427	9 US-09-918-995-17725	Sequence 578, App
C	31	15.2	76.0	791	10 US-09-832-849A-578	Sequence 370, App
C	32	15.2	76.0	1002	10 US-09-770-845-230	Sequence 1633, App
C	33	15.2	76.0	1828	10 US-09-917-800A-1643	Sequence 79, App
C	34	15.2	76.0	14831	10 US-09-669-08-79	Sequence 2116, App
C	35	15.2	76.0	14581	10 US-09-954-456-2116	Sequence 6887, App
C	36	15.2	75.0	442	9 US-10-040-862-6887	Sequence 3867, App
C	37	15.2	75.0	442	9 US-10-040-862-6887	Sequence 3867, App
C	38	15.2	75.0	485	9 US-09-795-692-3667	Sequence 3867, App
C	39	15.2	75.0	485	9 US-10-040-862-3867	Sequence 3867, App
C	40	15.2	75.0	504	9 US-09-766-692-8497	Sequence 8497, App
C	41	15.2	75.0	504	9 US-10-040-862-8497	Sequence 8497, App
C	42	15.2	75.0	1789	9 US-09-924-340-109	Sequence 109, App
C	43	15.2	75.0	1789	9 US-09-924-340-109	Sequence 391, App
C	44	14.8	74.0	365	9 US-09-924-340-109	Sequence 391, App
C	45	14.8	74.0	365	9 US-09-902-941-391	Sequence 391, App

RESULT 1	US-10-052-092-15	Sequence 176, App
	; Sequence 15, Application US710052092	Sequence 458, App
	; Publication No. US2003002778A1	Sequence 2874, App
	; GENERAL INFORMATION:	Applicant: Fuqua, Suzanne
		Applicant: Alred, D.
		Applicant: Hopp, Torsten A.
		Applicant: O'Connell, Peter
	; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapy	
	; FILE REFERENCE: P02102052	
	; CURRENT FILING DATE: 2002-01-18	
	; PRIOR APPLICATION NUMBER: US 60/262, 990	
	; PRIOR FILING DATE: 2001-01-19	
	; PRIOR FILING DATE: 2001-07-09	
	; NUMBER OF SEQ ID NOS: 49	
	; SOFTWARE: Patentin version 3.1	
	; SEQ ID NO 15	
	; LENGTH: 20	
	; TYPE: DNA	
	; ORGANISM: Artificial sequence	
	; FEATURE: OTHER INFORMATION: Primer	
	; US-10-052-092-15	
	Query Match	100.0%; Score 20; DB 9; Length 20;
	Best Local Similarity	100.0%; Pred. No. 0.82; Organization: CompaGen
	Matches	20; Conservative 0; Mismatches 0; Indels 0; caps 0;
	Db	1 CAAGGCCAGAGATGATG 20

RESULT 2
 US-10-052-092-4
 ; Sequence 4, Application US/10052092
 ; Publication No. US2003002778A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuqua, Suzanne

```

; APPLICANT: Allred, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeutic
; CURRENT APPLICATION NUMBER: US/10/052,092
; CURRENT FILING DATE: 2002-01-18
; PRIORITY APPLICATION NUMBER: US 60/262,990
; PRIORITY APPLICATION NUMBER: US 60/304,018
; PRIORITY FILING DATE: 2001-01-19
; PRIORITY FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Human
; US-10-052-092-4

Query Match 100.0%; Score 20; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.89; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGATGAG 20
Db 28 CAAGGCCAGAGATGAG 47

RESULT 3
US-10-052-092-3
; Sequence 3, Application US/10052092
; Publication No. US20030027778A1
; GENERAL INFORMATION:
; APPLICANT: Fuqua, Suzanne
; APPLICANT: Allred, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeutic
; FILE REFERENCE: P02102US2
; CURRENT APPLICATION NUMBER: US/10/052,092
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY APPLICATION NUMBER: US 60/262,990
; PRIORITY FILING DATE: 2001-01-19
; PRIORITY FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Human
; US-10-052-092-3

Query Match 100.0%; Score 20; DB 9; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.92; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGATGAG 20
Db 390 CAAGGCCAGAGATGAG 409

RESULT 4
US-10-052-092-4
; Sequence 4, Application US/10052092
; Publication No. US20030027778A1
; GENERAL INFORMATION:
; APPLICANT: Fuqua, Suzanne
; APPLICANT: Allred, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeutic
; FILE REFERENCE: P02102US2
; CURRENT APPLICATION NUMBER: US/10/052,092
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY APPLICATION NUMBER: US 60/262,990
; PRIORITY FILING DATE: 2001-01-19
; PRIORITY APPLICATION NUMBER: US 60/304,018
; PRIORITY FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Pig
; US-10-052-092-24

Query Match 100.0%; Score 20; DB 9; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0.93; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGATGAG 20
Db 801 CAAGGCCAGAGATGAG 820

RESULT 5
US-09-853-033-1
; Sequence 1, Application US/09853033
; Patent No. US20020100068A1
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, PIERRE
; APPLICANT: METZGER, DANIEL
; TITLE OF INVENTION: TRANSLUCINE MOUSE FOR TARGETED RECOMBINATION
; FILE REFERENCE: US05691J0222
; CURRENT APPLICATION NUMBER: US/09/853,033
; CURRENT FILING DATE: 2001-05-11
; PRIORITY APPLICATION NUMBER: FR 00/12570
; PRIORITY FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: CDS
; LOCATION: (1)..(1788)
; US-09-853-033-1

Query Match 100.0%; Score 20; DB 10; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0.93; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCCAGAGATGAG 20
Db 801 CAAGGCCAGAGATGAG 820

RESULT 6
US-10-052-092-6
; Sequence 6, Application US/10052092
; Publication No. US20030027778A1
; GENERAL INFORMATION:
; APPLICANT: Fuqua, Suzanne
; APPLICANT: Allred, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Methods and Composition in Breast Cancer Diagnosis and Therapeutic
; FILE REFERENCE: P02102US2
; CURRENT APPLICATION NUMBER: US/10/052,092
; PRIORITY FILING DATE: 2002-01-18
; PRIORITY APPLICATION NUMBER: US 60/262,990
; PRIORITY FILING DATE: 2001-01-19
; PRIORITY APPLICATION NUMBER: US 60/304,018
; PRIORITY FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Pig
; US-10-052-092-24

```

PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 6
LENGTH: 2092
TYPE: DNA
ORGANISM: Human
US-10-032-092-6

Query Match 100.0%; Score 20; DB 9; Length 2092;
Best Local Similarity 100.0%; Pred. No. 0.93; 0; Indels 0; gaps 0;
Matches 20; Conservative 0; Mismatches 0; DB 801 CAAAGGCCAGAGATGATG 820

RESULT 7
US-09-952-680A-9
Sequence 9, Application US/09952680A
Publication No. US20030087239A1
GENERAL INFORMATION:
APPLICANT: Stanton, Marty
APPLICANT: Epstein, David
APPLICANT: Hamaguchi, No. US20030087239A1
TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
FILE REFERENCE: 23239-501
CURRENT APPLICATION NUMBER: US/09/952,680A
CURRENT FILING DATE: 2001-09-13
PRIORITY APPLICATION NUMBER: 60/232,454
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 9
LENGTH: 2092
TYPE: DNA
ORGANISM: Homo sapiens
US-09-952-680A-9

RESULT 8
US-10-052-092-5
Query Match 100.0%; Score 20; DB 9; length 2092;
Best Local Similarity 100.0%; Pred. No. 0.93; 0; Mismatches 0; Indels 0; gaps 0;
Matches 20; Conservative 0; Mismatches 0; DB 801 CAAAGGCCAGAGATGATG 820

QY 1 CAAGGCCAGAGATGATG 20
Db 1093 CAAGGCCAGAGATGATG 1112

RESULT 9
US-09-281-674-9
Sequence 9, Application US/09281674
Patient No. US2002007730A1
GENERAL INFORMATION:
APPLICANT: Gossen, Manfred
Bujard, Hermann
Salfeld, Jochen
Voss, Jeffrey
TITLE OF INVENTION: Methods for Regulating Gene Expression
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Iahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
ZIP: 02109-1875
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/281,674
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,306
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/260,452
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: 08/076,327
FILING DATE: 14-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4963 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Human cytomegalovirus
IMMEDIATE SOURCE:
CLONE: PWD EGRA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-281-674-9

Query Match 100.0%; Score 20; DB 10; length 4963;
Best Local Similarity 100.0%; Pred. No. 0.95; 0; Indels 0; gaps 0;
Matches 20; Conservative 0; Mismatches 0; DB 1266 CAAAGGCCAGAGATGATG 1285
QY 1 CAAGGCCAGAGATGATG 20
Db 1266 CAAAGGCCAGAGATGATG 1285

SOFTWARE: PatentIn version 3.1
SEQ ID NO: 5
LENGTH: 2106
TYPE: DNA
ORGANISM: Human
US-10-032-092-5

RESULT 10
US-09-892-227-9
; Sequence 9, Application US/0989227
; Patent No. US2002015247A1
; GENERAL INFORMATION:
; APPLICANT: Gossen, Manfred
; Bujard, Jochen
; Salfeld, Hermann
; Voss, Jeffrey
; TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
; NUMBER OF SEQUENCES: 10
; NUMBER OF INVENTION: Transcriptional
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lablive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,227
; FILING DATE: 25-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/163,269
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/076,327
; FILING DATE: 14-Jun-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giulio A. DeConti, Jr.
; REFERENCE/DOCKET NUMBER: 31-503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-5941
; TELEX/FAX: (617) 227-400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4963 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human cytomegalovirus
; IMMEDIATE SOURCE:
; CLONE: PUDB BGR4
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
; US-09-892-227-9

RESULT 11
US-10-095-710-2
; Sequence 2, Application US/10096710
; Patent No. US2002016458A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Chawnshang
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
; DO NOT ATTENUATE THE PROTECTIVE EFFECTS OF ESTROGEN
; FILE REFERENCE: 22108.00102

RESULT 12
US-10-081-563-1
; Sequence 1, Application US/10081563
; Publication No. US20020187495A1
; GENERAL INFORMATION:
; APPLICANT: Wake Forest University
; APPLICANT: Heirington, David M.
; APPLICANT: Howard, Timothy D.
; APPLICANT: Hawkins, Gregory A.
; APPLICANT: Meyers, Deborah A.
; APPLICANT: Debora, Timothy D.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS OF ESTROGEN RECEPTOR ALPHA ASSOCIATED WITH
; FILE REFERENCE: 9151-15
; CURRENT APPLICATION NUMBER: US/10/081,563
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 6450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (361)..(2148)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESS NUMBER: X03635
; DATABASE ENTRY DATE: 1993-09-12
; RELEVANT RESIDUES: (1)..(6450)
; US-10-081-563-1

RESULT 13
US-10-052-092-1
; Sequence 1, Application US/10052092
; Publication No. US2003002778A1
; GENERAL INFORMATION:
; APPLICANT: Fuqia, Suzanne
; APPLICANT: Alired, D.
; APPLICANT: Hopp, Torsten A.
; APPLICANT: O'Connell, Peter

GenCore version 5.1.4_P5_4578
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 15:59:07 ; Search time 930.993 Seconds

(without alignments)
 347.918 Million cell updates/sec

Title: US-10-052-092-15

Perfect score: 20 caagcgccagagatgtg 20

Sequence: Sequence:

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em.estba:*

2: em.estbam:*

3: em.estbm:*

4: em.estml:*

5: em.estov:*

6: em.estpl:*

7: em.estro:*

8: em.htc:*

9: gb.estl:*

10: gb.estz:*

11: gb_htc:*

12: gb.est3:*

13: gb.esti:*

14: gb.est5:*

15: em.estfun:*

16: em.eston:*

17: gb.gss:*

18: em.gss_hum:*

19: em.gss_inv:*

20: em_gss_pln:*

21: em.gss_vrt:*

22: em.gss_fun:*

23: em_gss_mam:*

24: em.gss_mus:*

25: em.gss_other:*

26: em_gss_pro:*

em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	20	100.0	653 9 A1073549	A1073549 ov4e0e08 x
c 2	18.4	92.0	641 10 AW976636	AW976636 EST388745
c 3	18	90.0	642 12 BF058527	BF058527 7k31h08.x
c 4	17.4	87.0	687 10 BE513707	BE513707 601315475
c 5	17.4	87.0	771 17 AQ249357	AQ249357 T01818-SP
c 6	16.8	84.0	267 10 BE154100	BE154100 PMI-HT034

RESULT 1
 AI073549/
 LOCUS AI073549 653 bp mRNA linear EST 06-AUG-1998
 DEFINITION ov5eb0.xls Soares-testis_NBT Homo sapiens cDNA clone IMAGE:1640294
 ACCESSION AI073549
 VERSION AI073549.1 GI:3400193
 KEYWORDS EST;
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS NCI-CGAP
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabhsr@mail.nih.gov
 CGNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 Ph.D.
 CGNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at:
www.ncbi.nlm.nih.gov/ncicgap.
 www-bio.lnl.gov/biobp/image/image.html
 Seq primer: -40m13 fwd. ER from Amersham
 High quality sequence stop: 483.
 Location/Qualifiers

Source

1. .653

/organism="Homo sapiens"

Bf058527

LOCUS

Bf058527

DEFINITION

7431hb08.x1 NCI-CGAP_Ov18

mRNA

linear

EST

16-OCT-2000

/clone="MAGE:160294"

/clone_1lb="Soares-testis_NFM"

/sex="male"

/lab_host="DH10B"

/note="Vector: pMT3-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from Clontech Laboratories

, Inc., and primed with a Not I - oligo(dT) primer [5'

TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pMT3 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo.

"

BASE COUNT

151 a

169 c

142 g

181 t

ORIGIN

Query Match

Best Local Similarity

100.0%

Score 20;

DB 9;

Length 653;

Matches

20;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Db

612

CAAGGCCAGAGATG

593

RESULT 2

AM976536

LOCUS

AM976536

DEFINITION

EST_02-JUN-2000

VERSION

AM976536.1

EST:

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 642)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@nci.nih.gov

Tissue Procurement: Christopher A. Moskalk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. cDNA library Preparation: M. Bento

Soares, Ph.D. cDNA Library Arrayed by: Christa Range, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL, send email to:

<http://cgap.nci.nih.gov>

Seq primer: -40pm from Gibco

High quality sequence stop: 492.

FEATURES

source

1..642

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3477350"

/clone_1lb="NCI-CGAP_Ov18"

/tissue_type="Fibrobloma"

/lab_host="DH10B (Phage-resistant)"

/note="Organ: ovary; Vector: pMT3-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTTTT 3'];

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pMT3 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo.

"

BASE COUNT

158 a

182 c

196 g

106 t

ORIGIN

Query Match

Best Local Similarity

100.0%

Score 18;

DB 12;

Length 642;

Matches

18;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Db

609

CAAGGCCAGAGATGA

626

RESULT 4

BE513707

LOCUS

BE513707

DEFINITION

60115475FL NIH_MGC_8

mRNA

sequence

EST

07-AUG-2000

VERSION

BE513707.1

EST:

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 687)

NIH-MGC <http://mgc.nci.nih.gov/>

AUTHORS

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

Query Match 92.0%; Score 18.4; DB 10; Length 641; Best Local Similarity 95.0%; Pred. No. 1.9e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0; ORIGIN /db_xref="taxon:9606" /clone="MAGE resequences", "MAGN" /note="Vector: pBluescriptSKM"

BASE COUNT 159 a 175 c 195 g 112 t

Query Match 100.0%; Score 20; DB 9; Length 653; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ORIGIN /db_xref="taxon:9606" /clone="MAGE resequences", "MAGN" /note="Vector: pMT3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories , Inc., and primed with a Not I - oligo(dT) primer [5' TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 151 a 169 c 142 g 181 t

Query Match 100.0%; Score 20; DB 9; Length 653; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ORIGIN /db_xref="taxon:9606" /clone="MAGE resequences", "MAGN" /note="Vector: pMT3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories , Inc., and primed with a Not I - oligo(dT) primer [5' TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 158 a 182 c 196 g 106 t

Query Match 90.0%; Score 18; DB 12; Length 642; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ORIGIN /db_xref="taxon:9606" /clone="MAGE resequences", "MAGN" /note="Vector: pMT3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 158 a 182 c 196 g 106 t

Query Match 90.0%; Score 18; DB 12; Length 642; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ORIGIN /db_xref="taxon:9606" /clone="MAGE resequences", "MAGN" /note="Vector: pMT3-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TCTTACCACTCTGAGGGGGCCCAATTTCCTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

JOURNAL	Unpublished (1999)	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-mail.nih.gov
TISSUE		CDNA Library Preparation:	Ling Hong/Rubin Laboratory
CDNA LIBRARY PREPARATION		DNA Sequencing by:	Incyte Genomics, Inc.
Clone distribution:	MGC clone distribution information can be found through the T.I.M.A.G.E. Consortium/LLNL at: image.llnl.gov.	Plate:	LICM328 row: e column: 19
High quality sequence start:	6	High quality sequence stop:	441.
FEATURES	Location/Qualifiers	source	
BASE COUNT	281	a	154 c 108 g 201 t 27 others
ORIGIN			
Query Match	87.0%	Score	17.4; DB 17; Length 771;
Best Local Similarity	94.7%	Pred. No.	6.5e+02;
Matches	18;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CAAGGCCAGAGAAGCT 19		
Db	73 CAAGGTGAGAGATGAT 55		
RESULT 5			
BASE COUNT	184	a	176 c 207 g 120 t
ORIGIN			
Query Match	87.0%	Score	17.4; DB 10; Length 687;
Best Local Similarity	94.7%	Pred. No.	6.e+02;
Matches	18;	Mismatches	1; Indels 0; Gaps 0;
QY	2 AACGGCCAGAGATGAG 20		
Db	663 AACGGCCAGAGATGAG 681		
RESULT 5			
LOCUS	AQ249357		
DEFINITION	T10H18-SP6	71 bp	DNA linear
ACCESSION	AQ249357	GSS 06-oct-1998	
VERSION	AQ249357.1	GI:3699440	
KEYWORDS			
SOURCE			
ORGANISM	Arabidopsis thaliana		
Bukay-Yarai, Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. (bases 1 to 771)			
REFERENCE	Ecker, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.		
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 organism="Arabidopsis thaliana"		
Db	xref="taxon:3702"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	6	a	6 b 6 c 6 d 6 e 6 f
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	
BASE COUNT	67	a	63 c 77 g 60 t
ORIGIN			
Query Match	84.0%	Score	16.8; DB 10; Length 267;
Best Local Similarity	90.0%	Pred. No.	6.9e+02;
Matches	18;	Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 /clone="T10H18"		
Db	/clone_id="T10H18"		
FEATURES	Location/Qualifiers	source	</

QY	1 CAAGGCCGAGAGATGTG 20 127	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 327)
RESULT 7		
AW354950_c		
LOCUS	AW354950	319 bp mRNA linear EST 25-APR-2001
DEFINITION	37558 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.	
ACCESSION	AW354950	
VERSION	AW354950.1	GI:6833940
KEYWORDS	EST.	
SOURCE	COW.	
ORGANISM	Bos taurus	
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bovinae; Bos.	
REFERENCE	1 (bases 1 to 319), Smith,T.P.L., Grossie,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrkenring,S.C., Bennett, 'G.L., Heaton,M.P., Laegried,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I.I., Karamycheva,S., Liang,F., Quackenbush,J. and Keeler,J.W.	
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	
JOURNAL	Genome Res. 11 (4), 626-630 (2001)	
MEDLINE	2118013	
COMMENT	Contact: Smith TPL USA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68333-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov	
FEATURES		
source	FORWARD: AGGAACAGCTAAGCCAT BACKWARD: GTTTCCCCAGTCAGCG Plate: 22 row: J column: 16 Seq primer: ATTTAGGGACCATATAG. Location/qualifiers: 1. .319	
	/organism="Bos taurus" /db_xref="taxon:9013" /clone_id="MARC 1BOV" 'tissue_type="pooled" /lab_name="DHL0B"	
	<i>(note:-Vector: pcMV sport6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from lymph node, ovary, fat, Hypothalamus, and pituitary.)</i>	
BASE COUNT	86 a 88 c 65 g 86 t 2 others	
ORIGIN		
Query Match	84.0%; Score 16.8; DB 13; Length 327;	
Best Local Similarity	90.0%; Pred. No. 7.7e+02;	
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 CAAGGCCGAGAGATGTG 20	
Db	302 CAAGGCCGAGAGATGTG 283	
RESULT 9		
BB593363	BB593363	
LOCUS	BB593363	370 bp mRNA linear EST 18-AUG-2000
DEFINITION	WS1_93_H01.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.	
ACCESSION	BB593363	
VERSION	BB593363	
KEYWORDS	EST.	
SOURCE	Sorghum.	
ORGANISM	Sorghum bicolor	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 370)	
REFERENCE	L.H.	
AUTHORS	Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt	
TITLE	An EST database from Sorghum: water-stressed plants	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860	
RESULT 8		
BM66907/c		
LOCUS	BM66907	327 bp mRNA linear EST 27-FEB-2002
DEFINITION	952042H04.x1 952 - BMS tissue from Walbot lab (reduced rRNA) Zea mays cDNA, mRNA sequence.	
ACCESSION	BM66907	
VERSION	BM66907.1	GI:18964264
EST.		
SOURCE	zea mays.	

	source
Fax:	706 583 0210
Email:	mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions	
below Phred quality 16. The threshold for highest quality sequence	
is 20.	
Seq primer: Polymix	
High quality sequence start: 6	
High quality sequence stop: 352	
POLY=A>No.	
Location/Qualifiers	
1. .310	
/organism="Sorghum bicolor"	
/db_xref="taxon:4558"	
/clone_lib="Water-stressed 1 (WS1)"	
/note="Organ: Mix of 5-week old plants on days 7 & 8 after	
water was withheld; Vector: Lambda Zap; Site_1: XbaI;	
Site_2: EcoRI; The library was made from poly-A mRNA in the	
cloning vector lambda ZAP II. Clones to be sequenced were	
prepared by mass excision."	
N COUNT	
100 a 76 c 103 g 90 t 1 others	
QY Match	
Local Similarity 90.0%; Score 16.8; DB 10; Length 370;	
ches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
R COUNT	
97/c	
BFR042797	
BP250002A10F10 Soares normalized bovine placenta	
clone BP250002A10F10 5', mRNA sequence.	
BF042797/	
BP042797.1 GI:10759852	
EST.	
Cow	
Bos taurus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
Mammalia; Buterina; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	
Bovidae; Bovine; Bos.	
1 (bases 1 to 386)	
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson	
, J.H., Boyle ESTs	
Unpublished (2000)	
Contact: Lewin, H. A.	
W. M. Reck Center for Comparative and Functional Genomics	
University of Illinois at Urbana-Champaign	
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL	
61801, USA	
Tel: 217 333 5398	
Fax: 217 244 5617	
Email: h-lewin@uiuc.edu	
Funding for cattle EST sequencing was provided by the USDA National	
Research Initiative, Animal Genome Resource Grant AG-99-3205-8534	
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED	
from Washington University Genome Center. Vector Trими G;	
Cross_Match from Washington University Genome Center PHRAP suite.	
This sequence is vector free and at least 200 bp in length. REPEAT	
IN THE SEQUENCE Low_complexity STRAND (+) ELEMENT GC_Rich LOCATION	
[30..81].	
PCR PRIMERS	
FORWARD: TATAGGACTCACTATAGGG	
BACKWARD: ATTACCCCTACAGTAAAG	
Insert Length: 386 Std Error: 0.00	
Plate: BP250002A10 row: F column: 10	
Seq primer: AGCGGATACAGTTACACGGGA	
High quality sequence stop: 386.	
BASE COUNT	
83 a 103 c 141 g 59 t	
ORIGIN	
Query Match	
Best Local Similarity 90.0%; Score 16.8; DB 12; Length 386;	
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	
1 CAAGGCCAGAGATGATG 20	
Db	
220 CGAGCGCCGAGAGATG 201	
COMMENT	
RESUT 11	
BH552907/c	
LOCUS	
BH0461TR BOHQ Brassica oleracea genomic clone BOHQ61, DNA	
DEFINITION	
SEQUENCE	
ACCESSION	
BH552907	
VERSION	
BH552907.1 GI:17804687	
KEYWORDS	
GSS.	
SOURCE	
ORGANISM	
Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; core eudicots;	
REFERENCE	
1 (bases 1 to 422)	
AUTHORS	
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.	
TITLE	
Whole genome shotgun sequencing of Brassica oleracea	
JOURNAL	
Unpublished (2001)	
COMMENT	
Other_GSS: BOHQ61TR	
Contact: Chris Town	
TIGR	
9712 Medical Center Drive, Rockville, MD 20850, USA.	
Tel: 301-838-3523	
Fax: 301-838-0208	
Email: ctown@tigr.org	
DNA is from a doubled haploid provided by Tom Osborn.	
Seq Primer: TR Class: sheared ends.	
FEATURES	
SOURCE	
1. .422	
/organism="Brassica oleracea"	
/strain="TOI0000B13"	
/db_xref="taxon:3712"	
/clone="BOHQ61"	
/clone_lib="BOHO"	
/note="Vector: PROS1; Site_1: BstXII; 2-3 kb sheared	
genomic DNA inserted into PROS1 using BstXII linkers"	
BASE COUNT	
120 a 108 c 94 g 100 t	
ORIGIN	
Query Match	
Best Local Similarity 90.0%; Score 16.8; DB 17; Length 422;	
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	
1 CAAGGCCAGAGATGATG 20	
Db	
62 CGAGCGCCGAGAGATG 43	

AW354964/c	AW354964	1BOV	Bos taurus	433 bp	mRNA	linear	EST	25-APR-2001
LOCUS	AW354964							
DEFINITION	37542 MARC	1BOV	Bos taurus	CDNA 5'	mRNA sequence.			
ACCESSION	AW354964							
VERSION	AW354964.1							
KEYWORDS	EST.							
SOURCE	COW.							
ORGANISM	Bos taurus							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;								
Bovidae; Bosinae; Bos;								
REFERENCE	1 (bases 1 to 433)							
AUTHORS	Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,							
Smith, E., Wray, J.E., White, J., Cho, J., Fahrnkurg, S.C., Bennett,								
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,								
Perretta, G., Holt, I., Karamycheva, S., Liang, H., Quackenbush, J. and								
Keele, J.W.								
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA							
JOURNAL	Genome Res.							
MEDLINE	11 (4), 626-630 (2001)							
COMMENT	Contact: Smith TPL							
21180013	USDA, ARS, US Meat Animal Research Center, NE 68933-0166, USA							
Fax:	402 762 4390							
PO Box 166, Clay Center, NE 68933-0166, USA								
Tel:	402 762 4366							
Email: smithe@mail.marc.usda.gov								
Single pass sequencing. Bases called and trimmed with phred								
v0.98904.e. Vector identified by cross_match with the -minscore 20								
and -minmatch 12 options.								
PCR Primers								
FORWARD: AGAACAGGATGCGAT								
BACKWARD: GATTCGACTCAGCG								
Plate: 22 row: G column: 18								
Seq Primer: ATTGGGCACTATAG.								
FEATURES	Location/Qualifiers							
SOURCE	1. .433							
ORGIN	/organism="Bos taurus"							
BASE COUNT	/db_xref="taxon:9013"							
111 a	/clone_id="MARC_1BOV"							
108 c	/tissue_type="pooled"							
151 g	/lab_host="DH10B"							
63 t	/note=Vector: PCMV SPORT6; Site_1: Noct; Site_2: Sall;							
	Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."							
RESULT	13							
BB848708	BB848708	438 bp	mRNA	linear	EST	26-NOV-2001		
LOCUS	BB848708	RIKEN full-length enriched, adult inner ear	Mus musculus					
DEFINITION	BB848708	CDNA clone F930004E21 5', mRNA sequence.						
ACCESSION	BB848708							
VERSION	BB848708.1							
KEYWORDS	EST.							
SOURCE	house mouse.							
ORGANISM	Mus musculus							
Bukiriyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
Mammalia; Eutheria; Rodentia; Scurogathini; Muridae; Mus.								
REFERENCE	1 (bases 1 to 438)							
AUTHORS	Akimura, T., Akakawa, T., Carrinchi, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,							
RESULT	14							
BB847728	BB847728	439 bp	mRNA	linear	EST	26-NOV-2001		
LOCUS	BB847728	RIKEN full-length enriched, adult male kidney	Mus musculus					
DEFINITION	BB847728	CDNA clone F53010F07 5', mRNA sequence.						
ACCESSION	BB847728							
VERSION	BB847728.1							
KEYWORDS	EST.							
RESULT	14							
BB847728	BB847728	438 bp	mRNA	linear	EST	25-APR-2001		
LOCUS	BB847728	RIKEN full-length enriched, adult inner ear	Mus musculus					
DEFINITION	BB847728	CDNA clone F930004E21 5', mRNA sequence.						
ACCESSION	BB847728							
VERSION	BB847728							
KEYWORDS	EST.							
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, D., Sasaki, H., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akaihira, S., Tanaka, T., Tomaru, A., Toyoda, A., Watanuki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.								
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akiumura, T., et al. 2001)								
Unpublished (2001)								
Contact: Yoshihide Hayashizaki								
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute								
The Institute of Physical and Chemical Research (RIKEN)								
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan								
Tel: 81-45-503-9222								
Fax: 81-45-503-9215								
Email: genome-research.riken.go.jp/								
URL: http://genome.gsc.riken.go.jp/								
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okada, Y., Muramatsu, M., Hayashizaki, Y.								
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.								
Genome Res. 10 (10), 1617-1630 (2000)								
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okada, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.								
RIKEN Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)								
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 201-209 (2001)								
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.								
• mouse tissues.								
FEATURES	Location/Qualifiers							
SOURCE	1. .438							
ORGIN	/organism="Mus musculus"							
BASE COUNT	/strains="C57BL/6J"							
110 a	/db_xref="taxon:10090"							
108 c	/clone="F930004E21"							
100 g	/tissue_type="inner ear"							
63 t	/dev_stage="adult"							
	/note="pooled tissues ; (tissue_type=cerebellum,							
	(tissue_type=neonate, sex=mixed), dev_stage=16 days neonate, sex=mixed)", (tissue_type=hippocampus, dev_stage=adult, sex=male), (tissue_type=whole body, dev_stage=adult, embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days embryo, sex=mixed)"							
RESULT	14							
BB847728	BB847728	438 bp	mRNA	linear	EST	26-NOV-2001		
LOCUS	BB847728	RICKEN full-length enriched, adult inner ear	Mus musculus					
DEFINITION	BB847728	CDNA clone F930004E21 5', mRNA sequence.						
ACCESSION	BB847728							
VERSION	BB847728							
KEYWORDS	EST.							
RESULT	14							
BB847728	BB847728	439 bp	mRNA	linear	EST	25-APR-2001		
LOCUS	BB847728	RICKEN full-length enriched, adult male kidney	Mus musculus					
DEFINITION	BB847728	CDNA clone F53010F07 5', mRNA sequence.						
ACCESSION	BB847728							
VERSION	BB847728							
KEYWORDS	EST.							

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	I (bases 1 to 439)
TITLE	RIKEN Encyclopedia of Mouse Full-Length cDNAs (Akimura,T., et al. 2001)
COMMENT	Contact: Yoshinide Hayashizaki laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-research.riken.go.jp/ http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okarai,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
FEATURES	RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Y., and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: Real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 201-209 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. e mouse tissues.
source	location/Qualifiers
1. .439	
/organism="Mus musculus"	
/db_xref="taxon:0090"	
/clone="F530101F07"	
/clone_id="RIKEN full-length enriched, adult male kidney"	
/sex="male"	
/tissue_type="kidney"	
/dev_stage="adult"	
/lab_host="SOLR"	
/note="Site_1: XbaI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGTCAGCTCAATATATTAACCCCCCCC 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGGTCAGCTCAATATATTAACCCCCCCC 3']. cDNA was cleaved with XbaI and SstI."	
BASE COUNT	98 a 118 c 145 g 78 t
ORIGIN	Query Match 84.0%; Score 15.8; DB 12; Length 441; Best Local Similarity 90.0%; Pred. No. 9.2e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 CAAGGCCAGAGATGATG 20
Db	105 CAAGGCCAGAGATGCGC 124
RESULT	15
DEFINITION	BP041001 BP250019B20D11 Soares normalized bovine placenta Bos taurus mRNA sequence.
ACCESSION	BP041001
VERSION	BP041001.1
DEFINITION	BP250019B20D11 441 bp mRNA linear EST 10-OCT-2000
LOCUS	BP250019B20D11 5'
REFERENCE	Bovidae; Bovinae; Bos.
AUTHORS	Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,I. and Larson,J.H.
TITLE	Bovine ESTs
JOURNAL	Unpublished (2000)
COMMENT	Contact: Lewin, H. A. W.M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu
FEATURES	Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG-99-3305-5334 to H.A. Lewin and J. E. Womack. Base Calling Quality Scores: PHRED from Washington University Genome Center. Vector Trimmig: Cross match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length. PCR Primers
source	
1. .441	
/organism="Bos taurus"	
/db_xref="taxon:9913"	
/clone="BP250019B20D11"	
/clone_id="Soares normalized bovine placenta"	
/sex="female"	
/lab_host="DIL08"	
/note="Organ: placenta; Vector: pRT13pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."	
BASE COUNT	119 a 102 c 151 g 68 t 1 others
ORIGIN	Query Match 84.0%; Score 15.8; DB 12; Length 441; Best Local Similarity 90.0%; Pred. No. 9.2e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 CAAGGCCAGAGATGATG 20
Db	108 CGAGGCCAGAGATGATG 89
SEARCH COMPLETED	Search completed: May 17, 2003, 02:53:47
QUERY MATCH	84.0%; Score 16.8; DB 10; Length 439;

Mon May 19 10:04:46 2003

us-10-052-092-15.rst

Page 8

Job time : 937.993 secs